



1 TCGAACTCAC TCACCTCCCC TCTCACCTCA CTGCCCTCAC CAGCCAGCCT  
51 CTTGTCAAGT GATCAGGCTG TCAACCAACT TCTCTAGGAT AAGGTTTCAG  
101 GTCAGCCTGT GTGTATAAGA CCAGTGCCAA GCCAGAAGCA GCAGAGACAA  
151 CAGTGAATGA CAAGGAGGGG CCATCCAATC CCTGCTGCCA CCTCCTGGGA  
201 TGGAGCCCTA GGGAGCCCCT GTGCTGCCCC TGCCGTGGCA GGA CTACAG  
251 CCCACCGCT GCACTGAAGC CCAGGGCTGT GGAGCAGCTC TCTCCTTGGA  
301 CTCCTCTCGG CCCTAAAGGG ACTGGGCAGA GCCTTCCAGG ACTATGGTTG  
351 GACTGAAGCC TTCAGACGTG CCTCCCACCA TGGCTGTGAA GTTCCTGGGG  
401 GCAGGCACAG CAGCCTGTTT TGCTGACCTC GTTACCTTTC CACTGGACAC  
451 AGCCAAGGTC CGCCTGCAGA TCCAGGGGGA GAACCAGGCG GTCCAGACGG  
501 CCCGGCTCGT GCAGTACCGT GGCGTGCTGG GCACCATCCT GACCATGGTG  
551 CGGACTGAGG GTCCCTGCAG CCCCTACAAT GGGCTGGTGG CCGGCCTGCA  
601 GCGCCAGATG AGCTTCGCCT CCATCCGCAT CGGCCTTTAC GACTCCGTCA  
651 AGCAGGTGTA CACCCCCAAA GGCGCGGACA ACTCCAGCCT CACTACCCGG  
701 ATTTTGGCCG GCTGCACCAC AGGAGCCATG GCGGTGACCT GTGCCAGCC  
751 CACAGATGTG GTGAAGGTCC GATTTTCAGGC CAGCATACAC CTCGGGCCAT  
801 CCAGGAGCGA CAGAAAATAC AGCGGGACTA TGGACGCCTA CAGAACCATC  
851 GCCAGGGAGG AAGGAGTCAG GGGCCTGTGG AAAGGAACTT TGCCCAACAT  
901 CATGAGGAAT GCTATCGTCA ACTGTGCTGA GGTGGTGACC TACGACATCC  
951 TCAAGGAGAA GCTGCTGGAC TATCACCTGC TCACTGACAA CTTCCCCTGC  
1001 CACTTTGTCT CTGCCTTTGG AGCCGGCTTC TGTGCCACAG TGGTGGCCTC  
1051 CCCGGTGGAC GTGGTGAAGA CCCGGTATAT GAACTCACCT CCAGGCCAGT  
1101 ACTTCAGCCC CCTCGACTGT ATGATAAAGA TGGTGGCCCA GGAGGGCCCC  
1151 ACAGCCTTCT ACAAGGGATT TACACCCTCC TTTTGTGCGTT TGGGATCCTG  
1201 GAACGTGGTG ATGTTCTGTA CCTATGAGCA GCTGAAACGG GCCCTGATGA  
1251 AAGTCCAGAT GTTACGGGAA TCACCGTTTT GAACAAGACA AGAAGGCCAC  
1301 TGGTAGCTAA CGTGTCCGAA ACCAGTTAAG AATGGAAGAA AACGGTGCAT

FIG.1A

1351 CCACGCACAC ATGGACACAG ACCCACACAT GTTTACAGAA CTGTTGTTTA  
1401 CTTGTTGCTG ATTCAAGAAA CAGAAGTAGA AGAGAGAGGA TTCTGGTCTT  
1451 CACTGCCATG CCTCAAGAAC ACCTTTGTTT TGCACTGACA AGATGGAAAA  
1501 TAAATTATAT TAATTTTTGA AACCCATTAG GCATGCCTAA TATTTAGGCA  
1551 AGAGAAAATA AACCAAGATA GATCCATTTG GACAAAATGG AAGGTTGGAG  
1601 ACGTGTATCC CCGTGAAATC TGGTCAGATA ATGAATGATA AGCAGGAAGG  
1651 ATGGCAAGCA CGGGACAGGA GGGGCCACACA ATGGAGTGGG AGATCAGCCA  
1701 CGGAGCCTGG AGGGACGCCA CCCAGCAACA CAGAGCTGGC GACTGCAGCT  
1751 GCACCATCAC ACATGCATCA TCAGCCTATT TGTAATATGT CTGCCACAGA  
1801 GAGTCCTTTG GGATTCTAGG AAACCCAAGG AACAAGAGAA AAAACTAGAG  
1851 CCTGTGCTAA AGAAGCCTGC TGGGCCCATG TGAGGCTGGG GTCGTAAATA  
1901 TTCCCCGACG AACTGAAGA ATCAAGAGGG CAGCCCCCAC TTCTCCTACA  
1951 AAATGGAGGG AGCCATCCCT TCCCTGTCCA CCTCACCAGG GGTGCTATGA  
2001 CATGCAAGTG AGAAGCTGGG CATGAACGCA CTTTATAAAA GCAAAAGCTC  
2051 TGTGTAAATC TAACTACAAG GACAATGCCT TGGGAGAGAT TTTGTCGGGA  
2101 CAGAGAGGAG TTGCCAGGGA AGAAGGTTTG AAAGATACGG TTGTCTAGAG  
2151 GTGAGACCAA AGGATCCAGA GACTTGGGGA CCAGAGGTGA CAGTGGATGA  
2201 CGTGAAGCCA CAGGAGCCCC ACCCCCATGC AGCTTTTTTCC CCACCCCCC  
2251 CACCACGCGC TCAATCATGA GTACCTCAAA GGATTGTTGG GCTTGGGGGA  
2301 AAAGAGGTGG ATTCCTGGGC AGAACCTAA AGTAGCAGGA (SEQ ID NO.11)

**FIG.1B**

1 TCGAACTCACTCACCTCCCCTCTCACCTCACTGCCCTCACCAGCCAGCCTCTTGTCAAGT 60  
-----+-----+-----+-----+-----+  
AGCTTGAGTGAGTGGAGGGAGAGTGGAGTGACGGGAGTGGTGGTTCGGTTCGGAGAACAGTTCA  
  
61 GATCAGGCTGTCAACCAACTTCTCTAGGATAAGGTTTCAGGTGAGCCTGTGTGTAAGA 120  
-----+-----+-----+-----+-----+  
CTAGTCCGACAGTTGGTTGAAGAGATCCTATTCCAAAGTCCAGTCCGACACACATATTCT  
  
121 CCAGTGCCCAAGCCAGAGCAGAGACAAACAGTGAATGACAAGGAGGGGCCATCCAATC 180  
-----+-----+-----+-----+-----+  
GGTCACGGTTCGGTCTTCGTGCTCTGTGTGTCACTTACTGTCTCCTCCCGGTACCTTAG  
  
181 CCTGTGCCACCTCCTGGGATGGAGCCCTAGGGAGCCCCGTGTGTGCCCTGCCGTGGCA 240  
-----+-----+-----+-----+-----+  
GGACGACGGTGGAGGACCCTACCTCGGGATCCCTCGGGGACACGACGGGGACGGCACCGT  
  
241 GGA CTACAGCCCCACCGCTGCACTGAAGCCAGGCTGTGGAGAGCTCTCTCCTTGA 300  
-----+-----+-----+-----+-----+  
CCTGAGTGTGGGGTGGCGACGTGACTTCGGGTCCCGACACCTCGTCGAGAGAGGAACCT  
  
301 CTCCTCTCGGCCCTAAAGGGACTGGGCAGAGCCTTCCAGGACTATGGTTGGACTGAAGCC 360  
-----+-----+-----+-----+-----+  
GAGGAGAGCCGGGATTTCCCTGACCCGCTCTCGGAAGTCTGTATACCAACCTGACTTCGG  
M V G L K P  
TTCAGACGTGCCTCCACCATGGCTGTGAAGTTCCTGGGGGAGGCACAGCAGCCTGTTT  
  
361 AAGCTGCACGGAGGGTGGTACCGACACTTCAAGGACCCCGTCCGTGTGTCGGACAAA 420  
S D V P P T M A V K F L G A G T A A C F

FIG.2A

421 TGCTGACCTCGTTACCTTTCCACTGGACACAGCCAAGGTCGGCCTGCAGATCCAGGGGGA 480  
 -----+-----+-----+-----+-----+-----+  
 ACGACTGGAGCAATGGAAAGGTGACCTGTGTGGTTCCAGGGCGGACGTC TAGTCCCCCT  
 A D L V T F P L D T A K V R L Q I Q G E  
  
 461 GAACGAGGGGTCCAGACGGGCCGGCTCGTGCAGTACCGTGGCGTGTGGGCACCATCCT 540  
 -----+-----+-----+-----+-----+-----+  
 CTTGGTCCGCCAGGTCTGCCGGGCCGAGCAGTCATGGCACCGCACGCCGTTGGTAGGA  
 N Q A V Q T A R L V Q Y R G V L G T I L  
  
 541 GACCATGGTGGGACTGAGGGTCCCTGCAGGCCCTACAATGGGCTGGTGGCCGGCCTGCA 600  
 -----+-----+-----+-----+-----+-----+  
 CTGGTACCACGCCTGACTCCAGGGACGTCGGGGATGTTACCCGACCACCGCGCGGACGT  
 T M V R T E G P C S P Y N G L V A G L Q  
  
 601 GCGCCAGATGAGCTTCGCCTCCATCAGCATCGGCCTTTACGACTCCGTCAAGCAGGTGTA 660  
 -----+-----+-----+-----+-----+-----+  
 CGCGGTCTACTCGAAGCGGAGGTAGGCGTAGCCGGAAATGCTGAGGCAGTTCGTCCACAT  
 R Q M S F A S I R I G L Y D S V K Q V Y  
  
 661 CACCCCAAGGCGGACAACCTCCAGCCTCACTACCCGGATTTTGGCCGGCTGCACCAC 720  
 -----+-----+-----+-----+-----+-----+  
 GTGGGGGTTTCCGGCCCTGTTGAGGTGGAGTGGGCTAAACCGGCCGACGTGGTG  
 T P K G A D N S S L T T R I L A G C T T

FIG.2B

721 AGGAGCCATGGCGGTGACCTGTGCCCCAGCCACAGATGTGGTGAAGTCCGATTTTCAGGC 780  
-----+-----+-----+-----+-----+-----+  
TCCTCGGTACCGCCACTGGACACGGGTGGGTGTCTACACCACTTCCAGGCTAAAGTCCG  
G A M A V T C A Q P T D V V K V R F Q A  
  
781 CAGCATACACCTCGGGCCATCCAGGAGCGACAGAAAAATACAGCGGGACTATGGACGCCTA 840  
-----+-----+-----+-----+-----+-----+  
GTCGTATGTGGAGCCCGGTAGGTCTCGCTGTCTTTTATGTCGCCCTGATACCTGCGGAT  
S I H L G P S R S D R K Y S G T M D A Y  
  
841 CAGAACCATCGCCAGGGAGGAAGGAGTCAGGGGCCCTGTGGAAAGGAACCTTTGCCCAACAT 900  
-----+-----+-----+-----+-----+-----+  
GTCTTGGTAGCGGTCCCTCCCTCAGTCCCGGACACCTTTCCTTGAAACGGGTTGTA  
R T I A R E E G V R G L W K G T L P N I  
  
901 CATGAGGAATGCTATCGTCAACTGTCTGAGGTGGTGACCTACGACATCCTCAAGGAGAA 960  
-----+-----+-----+-----+-----+-----+  
GTACTCCTTACGATAGCAGTTGACACGACTCCACCACCTGGATGCTGTAGGAGTTCTCTT  
M R N A I V N C A E V V T Y D I L K E K  
  
961 GCTGTGGACTATCACCTGCTCACTGACAACCTCCCCCTGCCACTTGTGCTCTGCTTTGG 1020  
-----+-----+-----+-----+-----+-----+  
CGACGACCTGATAGTGGACGAGTGACTGTTGAAGGGGACGGTGAACACAGAGACGGAACCC  
L L D Y H L L T D N F P C H F V S A F G  
  
1021 AGCCGGCTTCTGTGCCACAGTGGTGGCCTCCCCGGTGGACGTGGTGAAGACCCGGTATAT 1080  
-----+-----+-----+-----+-----+-----+  
TCGGCCGAAGACACGGTGTCAACCACGGAGGGGCCACCTGCACCACCTTCTGGGCCATATA  
A G F C A T V V A S P V D V V K T R Y M

FIG.2C

1081 GAACTCACCTCCAGGCCAGTACTTCAGCCCCCTCGACTGTATGATAAAGATGGTGGCCCA 1140  
 -----+-----+-----+-----+-----+-----+  
 CTTGAGTGGAGGTCCGGTCATGAACTCGGGGGAGCTGACATACTATTICTACCACCGGGT  
 N S P P G Q Y F S P L D C M I K M V A Q  
  
 1141 GGAGGGCCCCACAGCCTTCTACAAGGATTTACACCCCTCCTTTTGGCGTTGGGATCCTG 1200  
 -----+-----+-----+-----+-----+-----+  
 CCTCCCGGGGTGTCGGAAGATGTTCCCTAAATGTGGGAGGAAAAACGCAAAACCCTAGGAC  
 E G P T A F Y K G F T P S F L R L G S W  
  
 1201 GAACGTGGTGATGTTCGTAACCTATGAGCAGCTGAAACGGGCCCTGATGAAAGTCCAGAT 1260  
 -----+-----+-----+-----+-----+-----+  
 CTTGCACCACTACAAGCATTGGATACTCGTCGACTTTGCCCGGGACTACTTTCAGGTCTA  
 N V V M F V T Y E Q L K R A L M K V Q M  
  
 1261 GTTACGGGAATCACCGTTTTGAACAAGACAAGAAGGCCACTGGTAGCTAACGTGTCCGAA 1320  
 -----+-----+-----+-----+-----+-----+  
 CAATGCCCTTAGTGGCAAAACTTGTTCTGTCTTCGGGTGACCATCGATTGCACAGGCTT  
 L R E S P F \* (SEQ ID NO.12)  
  
 1321 ACCAGTTAAGAAATGGAAGAAAACGGTGCATCCACGCACACATGGACACAGACCCACACAT 1380  
 -----+-----+-----+-----+-----+-----+  
 TGGTCAATTCTTACCTTCTTTTGGCCACGTAGGTGGGTGTGTACCTGTGTCTGGGTGTGTA

FIG.2D

1381 GTTTACAGAACTGTTGTTTACTTGTGCTGATTCAAGAAACAGAGTAGAAGAGAGAGGA  
 -----+-----+-----+-----+-----+ 1440  
 CAAATGCTTTGACAACAAATGAACAACGACTAAGTTCTTTGTCTTCATCTTCTCTCTCCT  
  
 1441 TTCTGGTCTTCACTGCCATGCCTCAAGAACACCTTTGTTTTGCACTGACAAGATGGAAAA  
 -----+-----+-----+-----+-----+ 1500  
 AAGACCAGAAAGTGACGGTACGGAGTTCTTGTGGAACAAAACGTGACGTCTACCTTTT  
  
 1501 TAAATTATATTAATTTTGGAAACCCATTAGGCATGCCCTAATATTTAGGCAAGAGAAAAATA  
 -----+-----+-----+-----+-----+ 1560  
 ATTTAATATAATTAAAAACTTTGGGTAATCCGTACGGATTATAAATCCGTTCCTTTTAT  
  
 1561 AACCAAGATAGATCCATTTGGACAAAAATGGAAGGTGGAGACGTGTATCCCCGTGAAATC  
 -----+-----+-----+-----+-----+ 1620  
 TTGGTTCTATCTAGGTAAACCTGTTTACCTTCCAACCTCTGCACATAGGGGCACCTTTAG  
  
 1621 TGGTCAGATAATGAATGATAAGCAGGAAGGATGGCAAGCACGGGACAGGAGGGGCCACACA  
 -----+-----+-----+-----+-----+ 1680  
 ACCAGTCTATTACTTACTTACTTCTCCTTCCCTACCGTTGCGTCCCTGTCCTCCCGGGTGT  
  
 1681 ATGGAGTGGGAGATCAGCCACGGAGCCTGGAGGGACGCCACCCAGCAACACAGAGCTGGC  
 -----+-----+-----+-----+-----+ 1740  
 TACCTCACCCCTCTAGTCGGTGCCTCGGACCTCCCTGCGGTGGGTGTTGTGCTCGACCG  
  
 1741 GACTGCAGCTGCACCATCACACATGCATCATCAGCCTATTTGTAATATGCTGCCACAGA  
 -----+-----+-----+-----+-----+ 1800  
 CTGACGTCGACGTGGTAGTGTGTACGTAGTAGTCGGATAAACATTATACAGACGGTGTCT  
  
 1801 GAGTCCCTTTGGGATTCTAGGAACCCCAAGGAACAAGAGAAAAAACTAGAGCCTGTGCTAA  
 -----+-----+-----+-----+-----+ 1860  
 CTCAGGAAACCCCTAAGATCCTTTGGGTTCCTTGTCTCTTTTGTGATCTCGGACACGATT

**FIG.2E**

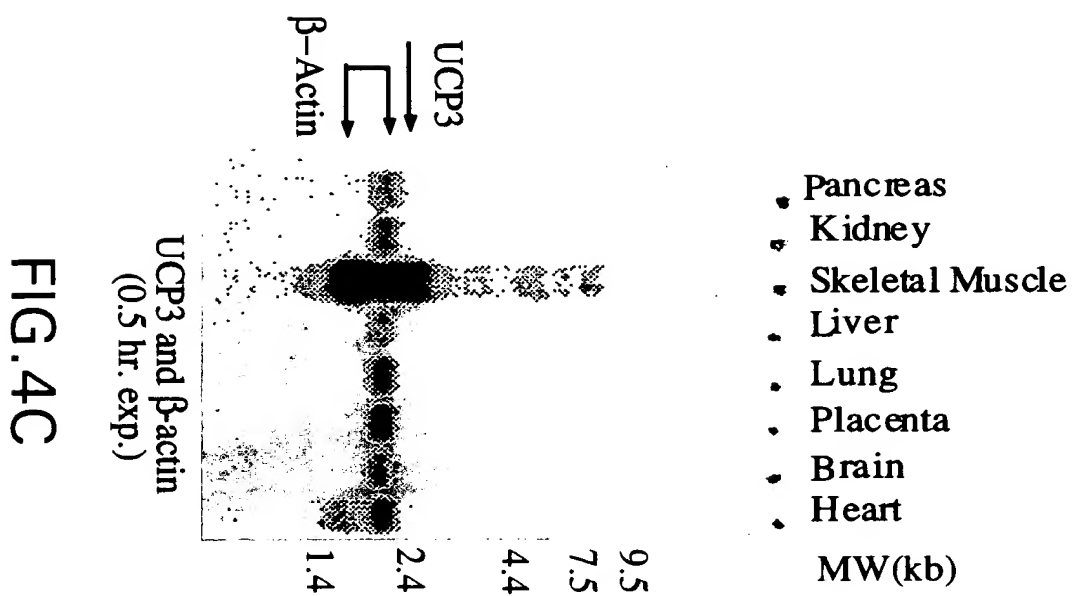
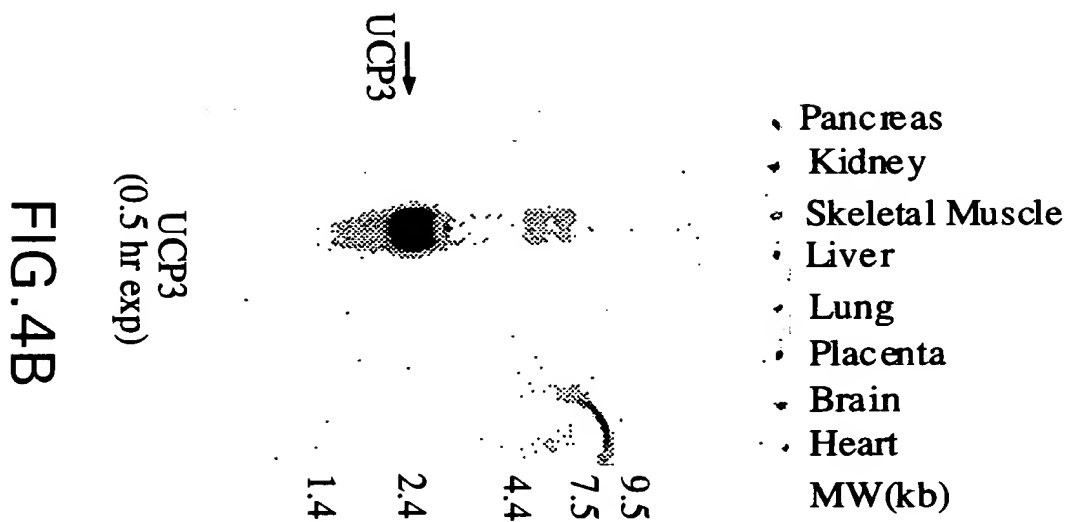
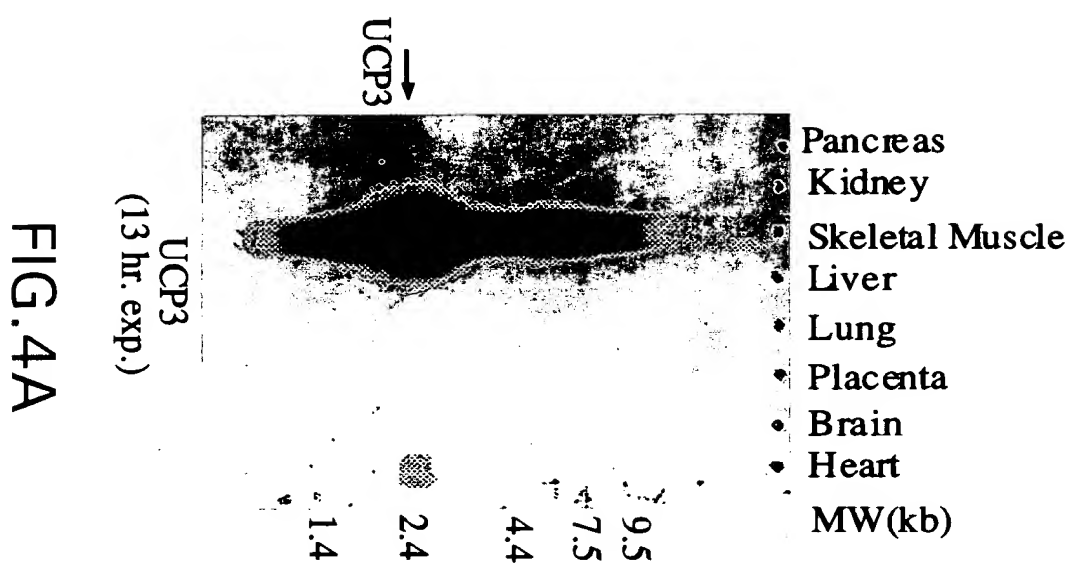
1861 AGAAGCCTGCTGGGCCCATGTGAGGCTGGGGTCGTAATAATTCCTCCGACGACACTGAAGA  
 -----+-----+-----+-----+-----+-----+ 1920  
 TCTTCGGACGACCCGGGTACACTCCGACCCAGCAATTTATAAGGGGCTGCTGTGACTTCT  
  
 1921 ATCAAGAGGGCAGCCCCACTTCTCTACAAAAATGGAGGGAGCCATCCCTTCCTGTCCA  
 -----+-----+-----+-----+-----+-----+ 1980  
 TAGTTCTCCCGTCGGGGTGAAGAGGATGTTTTACCTCCCTCGGTAGGGAAGGACAGGT  
  
 1981 CCTCACCAGGGTGCTATGACATGCAAGTGAGAAGCTGGGCATGAACGCACTTTATAAAA  
 -----+-----+-----+-----+-----+-----+ 2040  
 GGAGTGGTCCCCACGATACTGTAGGTTCACTCTTCGACCCGTACTTGCGTGAATATTTT  
  
 2041 GCAAAAGCTCTGTGTAATCTAACTACAAGGACAATGCCTTGGGAGAGATTTTGTGGGA  
 -----+-----+-----+-----+-----+-----+ 2100  
 CGTTTTCGAGACACATTTAGATTGATGTTCTCTGTTACGGAACCCCTCTCTAAACACAGCCCT  
  
 2101 CAGAGAGGAGTTGCCAGGGAAGGTTTGAAAGATACGGTTGCTAGAGGTGAGACCAA  
 -----+-----+-----+-----+-----+-----+ 2160  
 GTCTCTCCTCAACGGTCCCCTCTTCCAACTTCTATGCCAACAGATCTCCACTCTGGTT  
  
 2161 AGGATCCAGAGACTTGGGGACCAAGAGGTGACAGTGGATGACGTGAAGCCACAGGAGCCCC  
 -----+-----+-----+-----+-----+-----+ 2220  
 TCCTAGGTCTCTGAACCCCTGGTCTCCACTGTACCTACTGCACCTCGGTGTCCTCGGGG  
  
 2221 ACCCCCATGCAGCTTTTCCCAACCCCCCACCACGGCTCAATCATGAGTACCTCAAA  
 -----+-----+-----+-----+-----+-----+ 2280  
 TGGGGGTACGTGGA AAAAGGGGTGGGGGGGTGGTCCGCGAGTTAGTACTCATGGAGTTT  
  
 2281 GGATTGTTGGGCTTGGGGGAAAAGAGGTGGATTCTCTGGGCAAGAACCTAAAGTAGCAGGA  
 -----+-----+-----+-----+-----+-----+ 2340  
 CCTAACACCCGAACCCCTTTTCTCCACCTAAGGACCCGTTCTTGGAATTCATCGTCCT

**FIG.2F**



1 MVGLKPSSDP PTMAVKFLGA GTAACFADLV TFPLDTAKVR LQIQGENQAV  
51 QTARLVQYRG VLGITILTMVR TEGPCSPYNG LVAGLQRQMS FASIRIGLYD  
101 SVKQVYTPKG ADNSSLTTRI LAGCTTGAMA VTCAQPTDVV KVRFAQSIHL  
151 GPSRSDRKYS GTMDAYRTIA REEGVRGLWK GTLPNIMRNA IVNCAEVVTY  
201 DILKEKLLDY HLLTDNFPCH FVSAFGAGFC ATVVASPV DV VKTRYMNSPP  
251 GQYFSP LDCM IKMVAQEGPT AFYKGFTPSF LRLGSWNVVM FVTYEQLKRA  
301 LMKVQMLRES PF\* (SEQ ID NO.12)

**FIG.3**



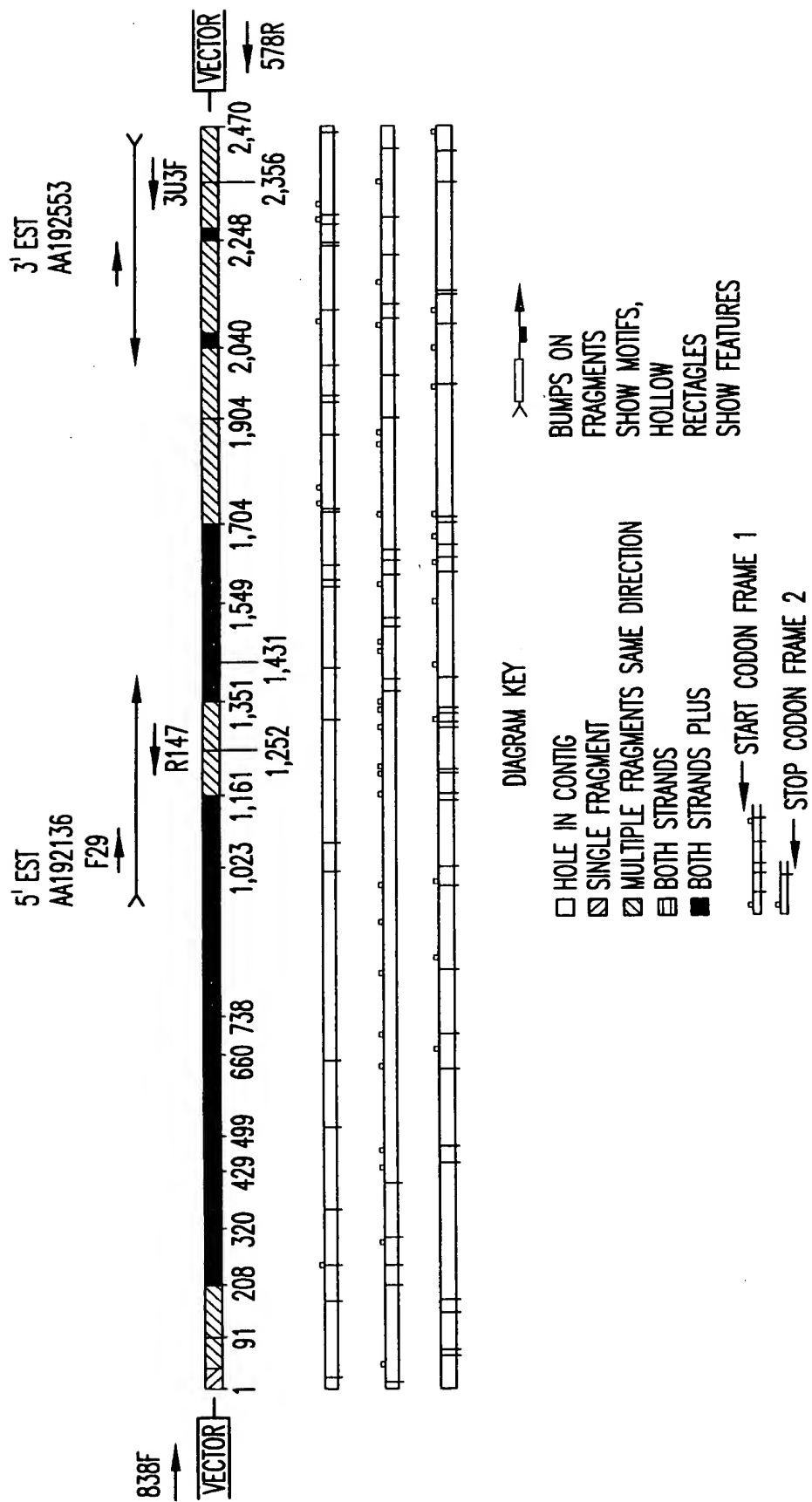


FIG.5

1 CCAGGAACAG CAGAGACAAC AGTGAATGGT GAGGCCCGGC CGTCAGATCC  
51 TGCTGCTACC TAATGGAGTG GATCCTTAGG GTCGCCCTGC ACTACCCAAC  
101 CTTGGCTAGA CGCACAGCTT CCTCCCTGAA CTGAAGCAAA AGATTGCCAG  
151 CCAAGCTCTC TCCTCGGACC TCCATAGGCA GCAAAGGAAC CAGGCCCAT  
201 CCCCAGGACC ATGGTTGGAC TTCAGCCCTC CGAAGTGCCT CCCACAACGG  
251 TTGTGAAGTT CCTGGGGGCC GGCCTGCGG CCIGTTTTGC GGACCTCCTC  
301 ACTTTTCCCC TGGACACCGC CAAGGTCCGT CTGCAGATCC AAGGGGAGAA  
351 CCCAGGGGCT CAGAGCGTGC AGTACCGCGG TGTGCTGGGT ACCATCCTGA  
401 CTATGGTGCG CACAGAGGGT CCCCAGAGCC CCTACAGCGG ACTGGTCGCT  
451 GGCCTGCACC GCCAGATGAG TTTTGCCTCC ATTCGAATTG GCCTCTACGA  
501 CTCTGTCAAG CAGTTCTACA CCCCCAAGGG AGCGGACCAC TCCAGCGTCG  
551 CCATCAGGAT TCTGGCAGGC TGCACGACAG GAGCCATGGC AGTGACCTGC  
601 GCCCAGCCCA CGGATGTGGT GAAGGTCCGA TTTCAAGCCA TGATACGCCT  
651 GGGAAGTGA GGAGAGAGGA AATACAGAGG GACTATGGAT GCCTACAGAA  
701 CCATCGCCAG GGAGGAAGGA GTCAGGGGCC TGTGGAAAGG GACTTGGCCC  
751 AACATCACAA GAAATGCCAT TGTCAACTGT GCTGAGATGG TGACCTACGA  
801 CATCATCAAG GAGAAGTTGC TGGAGTCTCA CCTGTTTACT GACAACTTCC  
851 CCTGTCACTT TGTCTCTGCC TTTGGAGCTG GCTTCTGTGC CACAGTGGTG  
901 GCCTCCCCGG TGGATGTGGT AAAGACCCGA TACATGAACG CTCCCCTAGG  
951 CAGGTACCGC AGCCCTCTGC ACTGTATGCT GAAGATGGTG GCTCAGGAGG

**FIG.6A**

1001 GACCCACGGC CTTCTACAAA GGATTTGTGC CCTCCTTTCT GCGTCTGGGA  
1051 GCTTGGAACG TGATGATGTT TGTAACATAT GAGCAACTGA AGAGGGCCTT  
1101 AATGAAAGTC CAGGTA CTGC GGAATCTCC GTTTTGAACA AGGCAAGCAG  
1151 GCTGCCTGGA ACAGAACAAA GCGTCTCTGC CCTGGGGACA CAGGCCCA  
1201 CGGTCCAGAA CCCTGCACTG CTGCTGACAC CAGAACTGA ACTAAAAGAG  
1251 GAGAGTTTTA GTCCTCCGTG TTTCGTCCTA AAACACCTCT GTTTTGCCT  
1301 GACCTGATGG GAAATAAATT ATATTAATTT TTAAACCCTT TCCGGTTGGA  
1351 TGCCTAACAT TTAGGCAAGA GACAACAAAG AAAACCAGAG TCAACTCCCT  
1401 TGAAATGTAG GAATAAAGGA TGCATAATAA ACAGGAAAGG CACAGGTTTT  
1451 GAGAAGATCA GCCCACAGTG TTGTCCTTGA ATCAAACAAA ATGGTCGGAG  
1501 GAACCCTTCG GGTTCAGCAC AAAGAGGTGA CTACAGCCTT TTGGTCACCA  
1551 GATGACTCCG CCCCTTTGTA ATGAGTCTGC CAAGTAGACT CTATCAAGAT  
1601 TCTGGGGAAA GGAGAAAGAA CACATTGACC TGCCCGGGCG GCCGCTCGAG  
1651 CCCTATGA (SEQ ID NO:17)

**FIG.6B**

1 MVGLQPSEVP PTTVVRFLGA GTAACFADLL TFPLDTAKVR LQIQGENPGA  
51 QSVQYRGVLG TILTMVRTEG PRSPYSGLVA GLHRQMSFAS IRIGLYDSVK  
101 QFYTPKGADH SSVAIRILAG CTTGAMAVTC AQPTDVVKVR FQAMIRLGTG  
151 GERKYRGTMD AYRTIAREEG VRGLWKGTWP NITRNAIVNC AEMVTYDIK  
201 EKLLESHLFT DNFPCHFVSA FGAGFCATVV ASPVDVVKTR YMNAPLGRRYR  
251 SPLHCMLKMV AQEGPTAFYK GFVPSFLRLG AWNVMMFVTY EQLRRALMKV  
301 QVLRESPF\* (SEQ ID NO:18)

**FIG.7**

FIG.8A

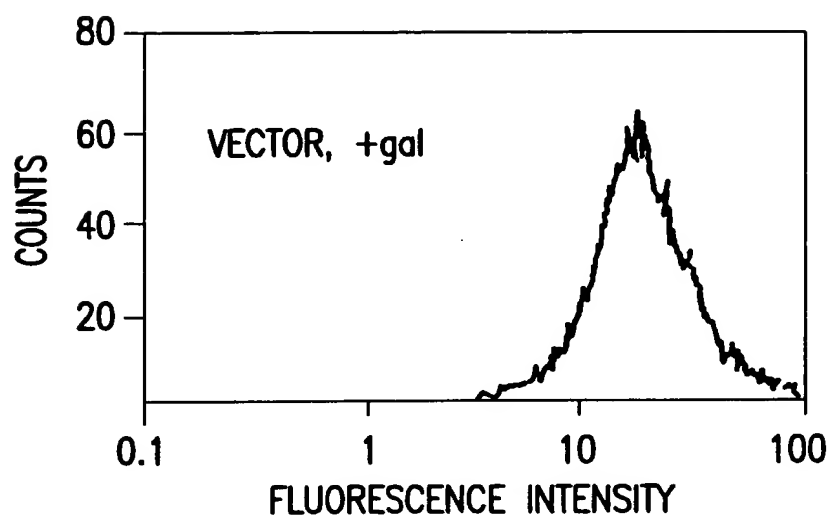


FIG.8B

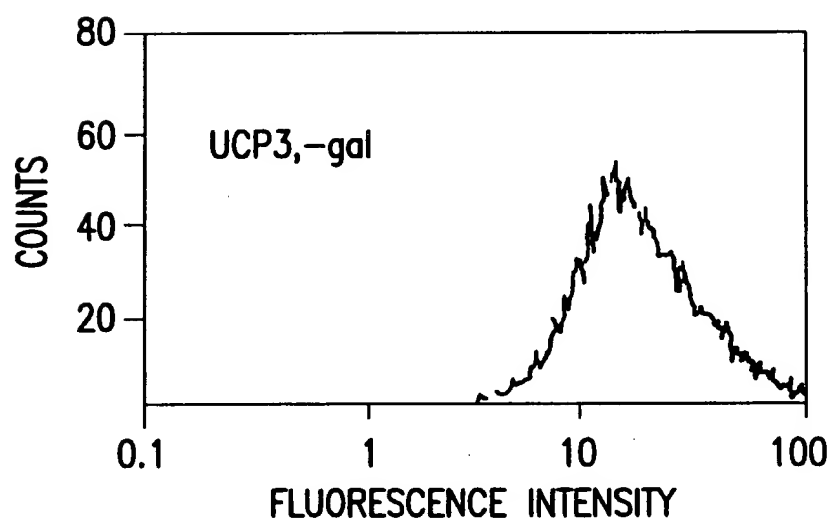
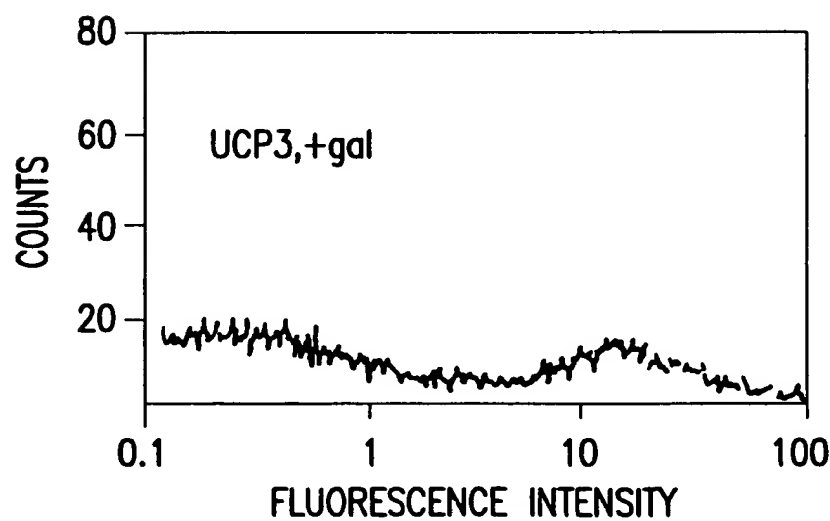


FIG.8C



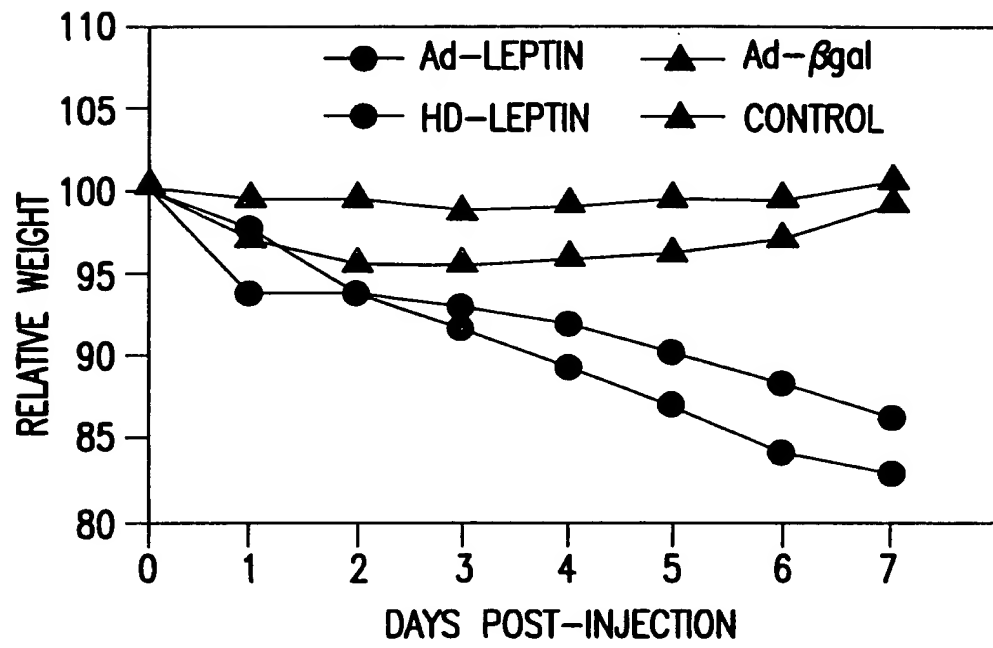


FIG.9A

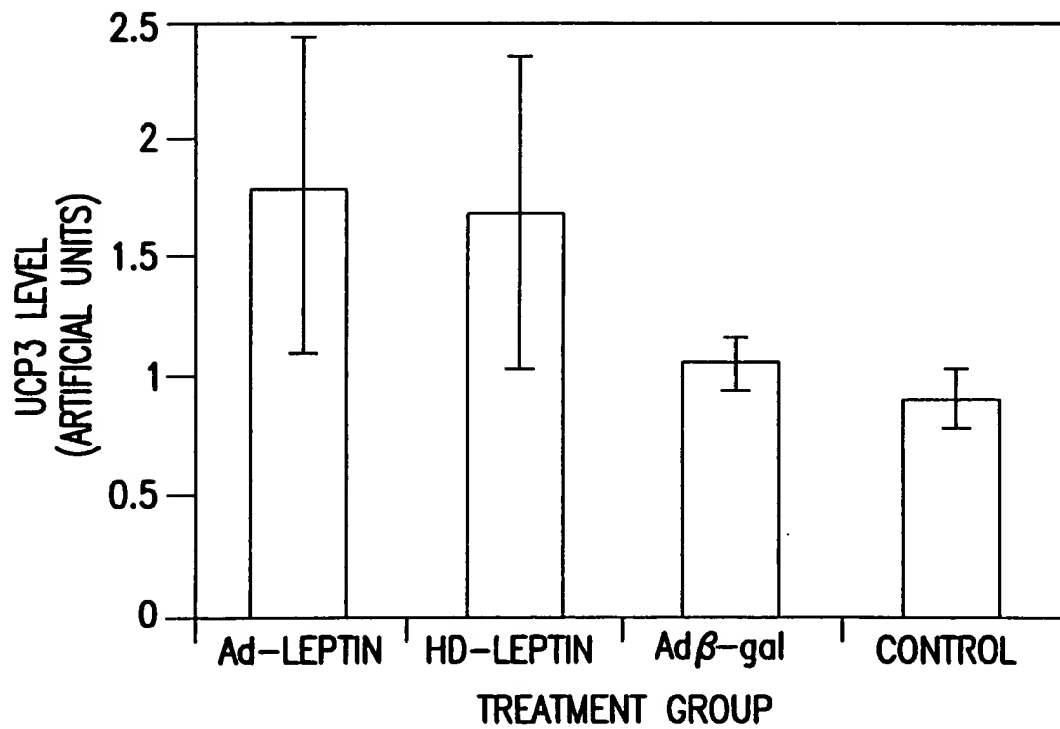


FIG.9B